<110> Gosling, Jennifer
Dairaghi, Daniel J.
Hanley, Michael
Miao, Zhenhua
Talbot, Dale
Schall, Thomas J.
ChemoCentryx, Inc.

<120> Chemokine Receptor

<130> 019934-0007210US

<140> US 09/721,495
<141> 2000-11-21

<150> US 60/159,015
<151> 1999-10-12

<150> US 60/159,210
<151> 1999-10-13

<150> US 60/172,979
<151> 1999-12-20

<150> US 60/173,388
<151> 1999-12-28

<150> US 60/186,626
<151> 2000-03-03

<150> US 09/686,019
<151> 2000-10-10

<160> 14

<170> PatentIn Ver. 2.1

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<220>
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<220>
<223> chemokine receptor CCX CKR

<400> 1

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Met Ala Leu Glu Gln Asn Gln Ser Thr Asp Tyr Tyr Tyr Glu Glu Asn
  1               5                  10                  15

gaa atg aat ggc act tat gac tac agt caa tat gaa ctg atc tgt atc   96
Glu Met Asn Gly Thr Tyr Asp Tyr Ser Gln Tyr Glu Leu Ile Cys Ile
             20                  25                  30
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aaa gaa gat gtc aga gaa ttt gca aaa gtt ttc ctc cct gta ttc ctc   144
Lys Glu Asp Val Arg Glu Phe Ala Lys Val Phe Leu Pro Val Phe Leu
          35                  40                  45

aca ata gtt ttc gtc att gga ctt gca ggc aat tcc atg gta gtg gca   192
Thr Ile Val Phe Val Ile Gly Leu Ala Gly Asn Ser Met Val Val Ala
     50                  55                  60

att tat gcc tat tac aag aaa cag aga acc aaa aca gat gtg tac atc   240
Ile Tyr Ala Tyr Tyr Lys Lys Gln Arg Thr Lys Thr Asp Val Tyr Ile
 65                  70                  75                  80

ctg aat ttg gct gta gca gat tta ctc ctt cta ttc act ctg cct ttt   288
Leu Asn Leu Ala Val Ala Asp Leu Leu Leu Leu Phe Thr Leu Pro Phe
                 85                  90                  95

tgg gct gtt aat gca gtt cat ggg tgg gtt tta ggg aaa ata atg tgc   336
Trp Ala Val Asn Ala Val His Gly Trp Val Leu Gly Lys Ile Met Cys
            100                 105                 110

aaa ata act tca gcc ttg tac aca cta aac ttt gtc tct gga atg cag   384
Lys Ile Thr Ser Ala Leu Tyr Thr Leu Asn Phe Val Ser Gly Met Gln
        115                 120                 125

ttt ctg gct tgt atc agc ata gac aga tat gtg gca gta act aaa gtc   432
Phe Leu Ala Cys Ile Ser Ile Asp Arg Tyr Val Ala Val Thr Lys Val
    130                 135                 140

ccc agc caa tca gga gtg gga aaa cca tgc tgg atc atc tgt ttc tgt   480
Pro Ser Gln Ser Gly Val Gly Lys Pro Cys Trp Ile Ile Cys Phe Cys
145                 150                 155                 160

gtc tgg atg gct gcc atc ttg ctg agc ata ccc cag ctg gtt ttt tat   528
Val Trp Met Ala Ala Ile Leu Leu Ser Ile Pro Gln Leu Val Phe Tyr
                165                 170                 175

aca gta aat gac aat gct agg tgc att ccc att ttc ccc cgc tac cta   576
Thr Val Asn Asp Asn Ala Arg Cys Ile Pro Ile Phe Pro Arg Tyr Leu
            180                 185                 190

gga aca tca atg aaa gca ttg att caa atg cta gag atc tgc att gga   624
Gly Thr Ser Met Lys Ala Leu Ile Gln Met Leu Glu Ile Cys Ile Gly
        195                 200                 205

ttt gta gta ccc ttt ctt att atg ggg gtg tgc tac ttt atc aca gca   672
Phe Val Val Pro Phe Leu Ile Met Gly Val Cys Tyr Phe Ile Thr Ala
    210                 215                 220

agg aca ctc atg aag atg cca aac att aaa ata tct cga ccc cta aaa   720
Arg Thr Leu Met Lys Met Pro Asn Ile Lys Ile Ser Arg Pro Leu Lys
225                 230                 235                 240

gtt ctg ctc aca gtc gtt ata gtt ttc att gtc act caa ctg cct tat   768
Val Leu Leu Thr Val Val Ile Val Phe Ile Val Thr Gln Leu Pro Tyr
                245                 250                 255

aac att gtc aag ttc tgc cga gcc ata gac atc atc tac tcc ctg atc   816
Asn Ile Val Lys Phe Cys Arg Ala Ile Asp Ile Ile Tyr Ser Leu Ile
            260                 265                 270
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acc agc tgc aac atg agc aaa cgc atg gac atc gcc atc caa gtc aca   864
Thr Ser Cys Asn Met Ser Lys Arg Met Asp Ile Ala Ile Gln Val Thr
        275                 280                 285

gaa agc atc gca ctc ttt cac agc tgc ctc aac cca atc ctt tat gtt   912
Glu Ser Ile Ala Leu Phe His Ser Cys Leu Asn Pro Ile Leu Tyr Val
    290                 295                 300

ttt atg gga gca tct ttc aaa aac tac gtt atg aaa gtg gcc aag aaa   960
Phe Met Gly Ala Ser Phe Lys Asn Tyr Val Met Lys Val Ala Lys Lys
305                 310                 315                 320

tat ggg tcc tgg aga aga cag aga caa agt gtg gag gag ttt cct ttt  1008
Tyr Gly Ser Trp Arg Arg Gln Arg Gln Ser Val Glu Glu Phe Pro Phe
                325                 330                 335

gat tct gag ggt cct aca gag cca acc agt act ttt agc att taa      1053
Asp Ser Glu Gly Pro Thr Glu Pro Thr Ser Thr Phe Ser Ile
            340                 345                 350

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aacatctgcc ttattctgaa aaaaaaaaaa aaam                             1147
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<210> 2
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<213> Homo sapiens

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<223> chemokine receptor CCX CKR

<400> 2

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Glu Met Asn Gly Thr Tyr Asp Tyr Ser Gln Tyr Glu Leu Ile Cys Ile
            20                  25                  30
Lys Glu Asp Val Arg Glu Phe Ala Lys Val Phe Leu Pro Val Phe Leu
        35                  40                  45
Thr Ile Val Phe Val Ile Gly Leu Ala Gly Asn Ser Met Val Val Ala
    50                  55                  60
Ile Tyr Ala Tyr Tyr Lys Lys Gln Arg Thr Lys Thr Asp Val Tyr Ile
65                  70                  75                  80
Leu Asn Leu Ala Val Ala Asp Leu Leu Leu Leu Phe Thr Leu Pro Phe
                85                  90                  95
Trp Ala Val Asn Ala Val His Gly Trp Val Leu Gly Lys Ile Met Cys
            100                 105                 110
Lys Ile Thr Ser Ala Leu Tyr Thr Leu Asn Phe Val Ser Gly Met Gln
        115                 120                 125
Phe Leu Ala Cys Ile Ser Ile Asp Arg Tyr Val Ala Val Thr Lys Val
    130                 135                 140
Pro Ser Gln Ser Gly Val Gly Lys Pro Cys Trp Ile Ile Cys Phe Cys
145                 150                 155                 160
Val Trp Met Ala Ala Ile Leu Leu Ser Ile Pro Gln Leu Val Phe Tyr
                165                 170                 175
Thr Val Asn Asp Asn Ala Arg Cys Ile Pro Ile Phe Pro Arg Tyr Leu
            180                 185                 190
Gly Thr Ser Met Lys Ala Leu Ile Gln Met Leu Glu Ile Cys Ile Gly
        195                 200                 205
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Phe Val Val Pro Phe Leu Ile Met Gly Val Cys Tyr Phe Ile Thr Ala
    210                 215                 220
Arg Thr Leu Met Lys Met Pro Asn Ile Lys Ile Ser Arg Pro Leu Lys
225                 230                 235                 240
Val Leu Leu Thr Val Val Ile Val Phe Ile Val Thr Gln Leu Pro Tyr
                245                 250                 255
Asn Ile Val Lys Phe Cys Arg Ala Ile Asp Ile Ile Tyr Ser Leu Ile
            260                 265                 270
Thr Ser Cys Asn Met Ser Lys Arg Met Asp Ile Ala Ile Gln Val Thr
        275                 280                 285
Glu Ser Ile Ala Leu Phe His Ser Cys Leu Asn Pro Ile Leu Tyr Val
    290                 295                 300
Phe Met Gly Ala Ser Phe Lys Asn Tyr Val Met Lys Val Ala Lys Lys
305                 310                 315                 320
Tyr Gly Ser Trp Arg Arg Gln Arg Gln Ser Val Glu Glu Phe Pro Phe
                325                 330                 335
Asp Ser Glu Gly Pro Thr Glu Pro Thr Ser Thr Phe Ser Ile
            340                 345                 350
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<210> 3
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<212> DNA
<213> Homo sapiens

<220>
<223> chemokine receptor CCX CKR (variant)

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aaagttttcc cccctgtatt cctcataata gttttcgtca ttggacttgc aggcaattcc 180
atggtagtgg caatttatgc ctattacaag aaacagagaa ccaaaacaga tgtgtacatc 240
ctgaatttgg ctgtagcaga tttactcctt ctattcactc tgccttttg ggctgttaat 300
gcagttcatg ggtgggtttt agggaaaata atgtgcaaaa taacttcagc cttgtacaca 360
ctaaactttg tctctggaat gcagtttctg gcttgtatca gcatagacag atatgtggca 420
gtaactaaag tccccagcca atcaggagtg ggaaaaccat gctggatcat ctgtttctgt 480
gtctggatgg ctgccatctt gctgagcata ccccagctgg ttttttatac agtaaatgac 540
aatgttaggt gcattcccat tttccccccgc aacttaggaa catcaatgaa agcattgatt 600
caaatgctag agatctgcat tggatttgta gtacccttc ttattatggg ggtgtgctac 660
tttatcacag caaggacact catgaagatg ccaaacatta aaatatctcg acccctaaaa 720
gttctgctca cagtcgttat agttttcatt gtcactcaac tgccttataa cattgtcaag 780
ttctgccgag ccatagacat catctactcc ctgatcacca gctgcaacat gagcaaacgc 840
atggacatcg ccatccaagt cacagaaagc atcgcactct ttcacagctg cctcaaccca 900
atcctttatg tttttatggg agcatctttc aaaaactacg ttatgaaagt ggccaagaaa 960
tatgggtcct ggagaagaca gagacaaagt gtggaggagt ttccttttga ttctgagggt 1020
cctacagagc caaccagtac ttttagcatt taaaggtaaa actgctctgc cttttgcttg 1080
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aaaaaam 1147

<210> 4
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 4
aatttggctg tagcagattt actcc 25

<210> 5
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 5
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<210> 6
<211> 369
<212> PRT
<213> Homo sapiens

<220>
<223> chemokine receptor CCR9

<400> 6

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            20                  25                  30
Phe Thr Asp Phe Tyr Cys Glu Lys Asn Asn Val Arg Gln Phe Ala Ser
        35                  40                  45
His Phe Leu Pro Pro Leu Tyr Trp Leu Val Phe Ile Val Gly Ala Leu
    50                  55                  60
Gly Asn Ser Leu Val Ile Leu Val Tyr Trp Tyr Cys Thr Arg Val Lys
65                  70                  75                  80
Thr Met Thr Asp Met Phe Leu Leu Asn Leu Ala Ile Ala Asp Leu Leu
                85                  90                  95
Phe Leu Val Thr Leu Pro Phe Trp Ala Ile Ala Ala Ala Asp Gln Trp
            100                 105                 110
Lys Phe Gln Thr Phe Met Cys Lys Val Val Asn Ser Met Tyr Lys Met
        115                 120                 125
Asn Phe Tyr Ser Cys Val Leu Leu Ile Met Cys Ile Ser Val Asp Arg
    130                 135                 140
Tyr Ile Ala Ile Ala Gln Ala Met Arg Ala His Thr Trp Arg Glu Lys
145                 150                 155                 160
Arg Leu Leu Tyr Ser Lys Met Val Cys Phe Thr Ile Trp Val Leu Ala
                165                 170                 175
Ala Ala Leu Cys Ile Pro Glu Ile Leu Tyr Ser Gln Ile Lys Glu Glu
            180                 185                 190
Ser Gly Ile Ala Ile Cys Thr Met Val Tyr Pro Ser Asp Glu Ser Thr
        195                 200                 205
Lys Leu Lys Ser Ala Val Leu Thr Leu Lys Val Ile Leu Gly Phe Phe
    210                 215                 220
Leu Pro Phe Val Val Met Ala Cys Cys Tyr Thr Ile Ile Ile His Thr
225                 230                 235                 240
Leu Ile Gln Ala Lys Lys Ser Ser Lys His Lys Ala Leu Lys Val Thr
                245                 250                 255
Ile Thr Val Leu Thr Val Phe Val Leu Ser Gln Phe Pro Tyr Asn Cys
            260                 265                 270
Ile Leu Leu Val Gln Thr Ile Asp Ala Tyr Ala Met Phe Ile Ser Asn
        275                 280                 285
Cys Ala Val Ser Thr Asn Ile Asp Ile Cys Phe Gln Val Thr Gln Thr
    290                 295                 300
Ile Ala Phe Phe His Ser Cys Leu Asn Pro Val Leu Tyr Val Phe Val
305                 310                 315                 320
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Gly Glu Arg Phe Arg Arg Asp Leu Val Lys Thr Leu Lys Asn Leu Gly
325 330 335
Cys Ile Ser Gln Ala Gln Trp Val Ser Phe Thr Arg Arg Glu Gly Ser
340 345 350
Leu Lys Leu Ser Ser Met Leu Leu Glu Thr Thr Ser Gly Ala Leu Ser
355 360 365
Leu

<210> 7
<211> 378
<212> PRT
<213> Homo sapiens

<220>
<223> chemokine receptor CCR7

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20 25 30
Ile Gly Asp Asn Thr Thr Val Asp Tyr Thr Leu Phe Glu Ser Leu Cys
35 40 45
Ser Lys Lys Asp Val Arg Asn Phe Lys Ala Trp Phe Leu Pro Ile Met
50 55 60
Tyr Ser Ile Ile Cys Phe Val Gly Leu Leu Gly Asn Gly Leu Val Val
65 70 75 80
Leu Thr Tyr Ile Tyr Phe Lys Arg Leu Lys Thr Met Thr Asp Thr Tyr
85 90 95
Leu Leu Asn Leu Ala Val Ala Asp Ile Leu Phe Leu Leu Thr Leu Pro
100 105 110
Phe Trp Ala Tyr Ser Ala Ala Lys Ser Trp Val Phe Gly Val His Phe
115 120 125
Cys Lys Leu Ile Phe Ala Ile Tyr Lys Met Ser Phe Phe Ser Gly Met
130 135 140
Leu Leu Leu Leu Cys Ile Ser Ile Asp Arg Tyr Val Ala Ile Val Gln
145 150 155 160
Ala Val Ser Ala His Arg His Arg Ala Arg Val Leu Leu Ile Ser Lys
165 170 175
Leu Ser Cys Val Gly Ser Ala Ile Leu Ala Thr Val Leu Ser Ile Pro
180 185 190
Glu Leu Leu Tyr Ser Asp Leu Gln Arg Ser Ser Ser Glu Gln Ala Met
195 200 205
Arg Cys Ser Leu Ile Thr Glu His Val Glu Ala Phe Ile Thr Ile Gln
210 215 220
Val Ala Gln Met Val Ile Gly Phe Leu Val Pro Leu Leu Ala Met Ser
225 230 235 240
Phe Cys Tyr Leu Val Ile Ile Arg Thr Leu Leu Gln Ala Arg Asn Phe
245 250 255
Glu Arg Asn Lys Ala Ile Lys Val Ile Ile Ala Val Val Val Val Phe
260 265 270
Ile Val Phe Gln Leu Pro Tyr Asn Gly Val Val Leu Ala Gln Thr Val
275 280 285
Ala Asn Phe Asn Ile Thr Ser Ser Thr Cys Glu Leu Ser Lys Gln Leu
290 295 300
Asn Ile Ala Tyr Asp Val Thr Tyr Ser Leu Ala Cys Val Arg Cys Cys
305 310 315 320
Val Asn Pro Phe Leu Tyr Ala Phe Ile Gly Val Lys Phe Arg Asn Asp
325 330 335

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Ile Phe Lys Leu Phe Lys Asp Leu Gly Cys Leu Ser Gln Glu Gln Leu
            340                 345                 350
Arg Gln Trp Ser Ser Cys Arg His Ile Arg Arg Ser Ser Met Ser Val
        355                 360                 365
Glu Ala Glu Thr Thr Thr Thr Phe Ser Pro
    370                 375


<210> 8
<211> 374
<212> PRT
<213> Homo sapiens

<220>
<223> chemokine receptor CCR6

<400> 8
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Asp Tyr Phe Val Ser Val Asn Thr Ser Tyr Tyr Ser Val Asp Ser Glu
             20                  25                  30
Met Leu Leu Cys Ser Leu Gln Glu Val Arg Gln Phe Ser Arg Leu Phe
         35                  40                  45
Val Pro Ile Ala Tyr Ser Leu Ile Cys Val Phe Gly Leu Leu Gly Asn
     50                  55                  60
Ile Leu Val Val Ile Thr Phe Ala Phe Tyr Lys Lys Ala Arg Ser Met
 65                  70                  75                  80
Thr Asp Val Tyr Leu Leu Asn Met Ala Ile Ala Asp Ile Leu Phe Val
                 85                  90                  95
Leu Thr Leu Pro Phe Trp Ala Val Ser His Ala Thr Gly Ala Trp Val
            100                 105                 110
Phe Ser Asn Ala Thr Cys Lys Leu Leu Lys Gly Ile Tyr Ala Ile Asn
        115                 120                 125
Phe Asn Cys Gly Met Leu Leu Leu Thr Cys Ile Ser Met Asp Arg Tyr
    130                 135                 140
Ile Ala Ile Val Gln Ala Thr Lys Ser Phe Arg Leu Arg Ser Arg Thr
145                 150                 155                 160
Leu Pro Arg Thr Lys Ile Ile Cys Leu Val Val Trp Gly Leu Ser Val
                165                 170                 175
Ile Ile Ser Ser Ser Thr Phe Val Phe Asn Gln Lys Tyr Asn Thr Gln
            180                 185                 190
Gly Ser Asp Val Cys Glu Pro Lys Tyr Gln Thr Val Ser Glu Pro Ile
        195                 200                 205
Arg Trp Lys Leu Leu Met Leu Gly Leu Glu Leu Leu Phe Gly Phe Phe
    210                 215                 220
Ile Pro Leu Met Phe Met Ile Phe Cys Tyr Thr Phe Ile Val Lys Thr
225                 230                 235                 240
Leu Val Gln Ala Gln Asn Ser Lys Arg His Lys Ala Ile Arg Val Ile
                245                 250                 255
Ile Ala Val Val Leu Val Phe Leu Ala Cys Gln Ile Pro His Asn Met
            260                 265                 270
Val Leu Leu Val Thr Ala Ala Asn Leu Gly Lys Met Asn Arg Ser Cys
        275                 280                 285
Gln Ser Glu Lys Leu Ile Gly Tyr Thr Lys Thr Val Thr Glu Val Leu
    290                 295                 300
Ala Phe Leu His Cys Cys Leu Asn Pro Val Leu Tyr Ala Phe Ile Gly
305                 310                 315                 320
Gln Lys Phe Arg Asn Tyr Phe Leu Lys Ile Leu Lys Asp Leu Trp Cys
                325                 330                 335
Val Arg Arg Lys Tyr Lys Ser Ser Gly Phe Ser Cys Ala Gly Arg Tyr
            340                 345                 350
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Ser Glu Asn Ile Ser Arg Gln Thr Ser Glu Thr Ala Asp Asn Asp Asn
        355                 360                 365
Ala Ser Ser Phe Thr Met
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<210> 9
<211> 342
<212> PRT
<213> Homo sapiens

<220>
<223> chemokine receptor STRL33

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Asp Ser Ser Gln Glu Glu His Gln Asp Phe Leu Gln Phe Ser Lys Val
             20                  25                  30
Phe Leu Pro Cys Met Tyr Leu Val Val Phe Val Cys Gly Leu Val Gly
         35                  40                  45
Asn Ser Leu Val Leu Val Ile Ser Ile Phe Tyr His Lys Leu Gln Ser
     50                  55                  60
Leu Thr Asp Val Phe Leu Val Asn Leu Pro Leu Ala Asp Leu Val Phe
 65                  70                  75                  80
Val Cys Thr Leu Pro Phe Trp Ala Tyr Ala Gly Ile His Glu Trp Val
                 85                  90                  95
Phe Gly Gln Val Met Cys Lys Ser Leu Leu Gly Ile Tyr Thr Ile Asn
            100                 105                 110
Phe Tyr Thr Ser Met Leu Ile Leu Thr Cys Ile Thr Val Asp Arg Phe
        115                 120                 125
Ile Val Val Val Lys Ala Thr Lys Ala Tyr Asn Gln Gln Ala Lys Arg
    130                 135                 140
Met Thr Trp Gly Lys Val Thr Ser Leu Leu Ile Trp Val Ile Ser Leu
145                 150                 155                 160
Leu Val Ser Leu Pro Gln Ile Ile Tyr Gly Asn Val Phe Asn Leu Asp
                165                 170                 175
Lys Leu Ile Cys Gly Tyr His Asp Glu Ala Ile Ser Thr Val Val Leu
            180                 185                 190
Ala Thr Gln Met Thr Leu Gly Phe Phe Leu Pro Leu Leu Thr Met Ile
        195                 200                 205
Val Cys Tyr Ser Val Ile Ile Lys Thr Leu Leu His Ala Gly Gly Phe
    210                 215                 220
Gln Lys His Arg Ser Leu Lys Ile Ile Phe Leu Val Met Ala Val Phe
225                 230                 235                 240
Leu Leu Thr Gln Met Pro Phe Asn Leu Met Lys Phe Ile Arg Ser Thr
                245                 250                 255
His Trp Glu Tyr Tyr Ala Met Thr Ser Phe His Tyr Thr Ile Met Val
            260                 265                 270
Thr Glu Ala Ile Ala Tyr Leu Arg Ala Cys Leu Asn Pro Val Leu Tyr
        275                 280                 285
Ala Phe Val Ser Leu Lys Phe Arg Lys Asn Phe Trp Lys Leu Val Lys
    290                 295                 300
Asp Ile Gly Cys Leu Pro Tyr Leu Gly Val Ser His Gln Trp Lys Ser
305                 310                 315                 320
Ser Glu Asp Asn Ser Lys Thr Phe Ser Ala Ser His Asn Val Glu Ala
                325                 330                 335
Thr Ser Met Phe Gln Leu
            340
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<210> 10
<211> 740
<212> DNA
<213> Homo sapiens

<220>
<223> DNA sequence 5' to the translation start site
of the CCX CKR gene

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tatttaactt atttaaatta aatttataaa taacatcaaa ataaaaaata aatttaattt 120
aaataaacca agtaatttgc tattttcgtt tttattcaat ttgttgtaga tatactttta 180
cgattcacaa aattatgtat gtaaagatta taacactatt tattcttttt agttaaaatc 240
taattaaatt ttcatatttt aaaaatcatt tttacataaa agtcttcact tttatttagg 300
atttaatgat taagaaaatt ctccagggca ttatgtttat tgtcctgttc aaatccaagc 360
tctttcacac agaattgtac aagcaaagtt tgagtaacta atcttggggt catattccaa 420
tgtggctccc attaaagcat ttcaaagagt gctagattca ggctcacata tgttacagca 480
acaggctata ctctagggaa agaacaaaac agcttgatag aaactgtgtg cttttaagca 540
tatttagaca aatatctatc ctgtattctc tttgccatct agattggagc catggctttg 600
gaacagaacc gtcaacagat tattattatg aggagaagtg aaatgaatgg cctgatgact 660
acagtcagta tgaactgatc tgttcagaga agagacagag gatatgcaca gggttgctcc 720
ctgtattgct caccatagag 740

<210> 11
<211> 347
<212> DNA
<213> Homo sapiens

<220>
<223> positions 1-347 of CXC CKR

<400> 11
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acttatgact acagtcaata tgaactgatc tgtatcaaag aagatgtcag agaatttgca 120
aaagttttcc tccctgtatt cctcacaata gttttcgtca ttggacttgc aggcaattcc 180
atggtagtgg caatttatgc ctattacaag aaacagagaa ccaaaacaga tgtgtacatc 240
ctgaatttgg ctgtagcaga tttactcctt ctattcactc tgccttttg ggctgttaat 300
gcagttcatg ggtgggtttt agggaaaata atgtgcaaaa taacttc 347

<210> 12
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:peptide
translation of non-coding region of SEQ ID NO:1

<400> 12
Asn Cys Ser Ala Phe Cys Leu Asp Thr Tyr Glu
1 5 10

<210> 13
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:peptide
translation of non-coding region of SEQ ID NO:1

<400> 13
Cys Phe Pro Leu Lys
1 5

<210> 14
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:peptide
translation of non-coding region of SEQ ID NO:1

<400> 14
Asn Ile Cys Leu Ile Leu Lys Lys Lys Lys Lys
1 5 10